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Seleção de populações de soja para precocidade e alta produtividade de grãos

Selection of soybean populations for earliness and high grain yield

Selección de poblaciones de soja para precocidad y alta productividad de granos

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Resumo

Os programas de melhoramento de soja brasileiros em sua maioria visam a obtenção de genótipos com ciclo precoce e alto rendimento de grãos. Assim, este estudo objetivou selecionar linhagens de soja precoces com alta produtividade para a região do Cerrado brasileiro. O experimento foi conduzido na safra 2017/2018 na Universidade Federal de Mato Grosso do Sul, Campus Chapadão do Sul, e consistiu de um delineamento de blocos aumentados usando 196 linhagens e dez controles, com cinco repetições para cada controle. Os caracteres avaliados foram altura de plantas, número de dias para o florescimento e produtividade de grãos. Após constatar a presença de variabilidade genética para todos os caracteres, avaliaram-se dois métodos de seleção: a seleção direta em cada caráter e a seleção simultânea (para reduzir a altura e o número de dias para o florescimento e aumentar a produtividade de grãos, usando o índice de Mulamba e Mock). Este último considerou dois cenários para estabelecer o peso econômico: o coeficiente de variação genotípico (CVg) e pesos arbitrários. A seleção direta sobre as variáveis teve resultados insatisfatórios. O índice de Mulamba e Mock revelou resultados insatisfatórios quando usando CVg como peso econômico e resultatos satisfatórios quando usando pesos arbitrários.

Palavras-chave: *Glycine max*; Melhoramento de plantas; Ganho genético; Índice de seleção; Seleção simultânea.

Abstract

Brazilian breeding programs usually aim at finding genotypes with early cycle and high grain yield. Thus, this study aimed to select early soybean lines with high grain yield for the Cerrado region. The experiment was carried out in the 2017-2018 season, in the Universidade Federal de Mato Grosso do Sul, Campus Chapadão do Sul, and consisted of an augmented blocks design, using 196 lines and ten controls, with five replications for each control. The experiment evaluated the traits plant height, number of days to flowering, and grain yield.

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After verifying the genetic variability for all traits, two selection methods were evaluated, the direct selection in each trait and the simultaneous selection (to decrease plant height and number of days to flowering and increase grain yield, using the Mulamba and Mock index). The latter considered two scenarios were when establishing the economic weight: the coefficient of genotypic variation (CVg) and arbitrary weights. Direct selection on the variables had unsatisfactory results. The Mulamba and Mock revealed unsatisfactory results when using CVg as the economic weight and satisfactory results when using arbitrary weights.

Keywords: *Glycine max*; Plant breeding; Genetic gain; Selection index; Simultaneous selection.

Resumen

Los programas de mejoramiento en Brasil generalmente buscan encontrar genotipos de ciclo precoz y alto rendimiento de granos. Por lo tanto, este estudio tuvo como objetivo seleccionar líneas de soja precoces con alto rendimiento de granos para la región de Cerrado. El experimento se llevó a cabo en la temporada 2017-2018, en la Universidade Federal de Mato Grosso do Sul, Campus Chapadão do Sul, y consistió en un diseño de bloques aumentados, utilizando 196 líneas y diez controles, con cinco réplicas para cada control. El experimento evaluó los caracteres altura de la planta, número de días para la floración y rendimiento de granos. Después de verificar la variabilidad genética de todos los caracteres, se evaluaron dos métodos de selección, la selección directa en cada carácter y la selección simultánea (para reducir la altura de la planta y número de días para la floración y aumentar el rendimiento de los granos, utilizando el índice de Mulamba y Mock). Estos últimos consideraron dos escenarios a la hora de establecer el peso económico: el coeficiente de variación genotípica (CVg) y los pesos arbitrarios. La selección directa sobre las variables tuvo resultados insatisfactorios. El índice de Mulamba y el Mock revelaron resultados insatisfactorios al utilizar el CVg como peso económico y resultados satisfactorios al utilizar pesos arbitrarios.

Palabras claves: *Glycine max*; Mejoramiento de plantas; Ganancia genética; Índice de selección; Selección simultánea.

1. Introduction

Soybean (*Glycine max* (L.) Merrill) is the main crop in Brazilian agriculture due to the high export demand. Its grains are widely used in human and animal feed owing to their high oil and protein content. World soybean production in the 2018/2019 harvest was approximately 338 million tons in a cultivated area of 124 million hectares (USDA, 2019). In the 2018/2019 season, the area planted with soybean corresponded to 35 million hectares of the Brazilian territory, and the grain yield reached approximately 3.2 t ha^{-1} (Conab, 2020). The national production in the last season was of about 115 million tons. Soybean cultivation areas in the country are predominantly in the Cerrado biome (Silva et al., 2017), which accounted for 61% of total soybean production (SojaMaps, 2020).

The economic importance of soybean crop in recent years is evident when analyzing its production history. In the past 18 years, grain production in Brazil increased from 38 million in the 2000/2001 season to over 119 million in the 2018/2019 season. These results are mostly due to breeding and adequate phytotechnical practices allied to the expansion of the cultivation area (Silva et al., 2017). However, Brazilian yield can still be increased when compared to that of the United States, the largest soybean producer in the world.

In Brazil, soybean breeding programs aim to create new cultivars with agronomic performance superior to those found in the market. Besides the high grain yield, breeders seek early soybean genotypes (Meotti et al., 2012). This is because farmers have the possibility of growing maize or cotton in the off-season, between February and July, in the Brazilian Cerrado. Water deficiency and photoperiod are some factors that can compromise the yield of crops grown in off-season (Sediyama, 2009).

The main traits to be evaluated for earliness are number of days to flowering and maturity. The literature reports ten genes involved in the genetic control of these traits (Watanabe et al., 2012; Jiang et al., 2014; Kong et al., 2014), which requires efficient breeding methods. Thus, the present study aimed to select early-cycle soybean lines with high grain yield for Brazilian Cerrado.

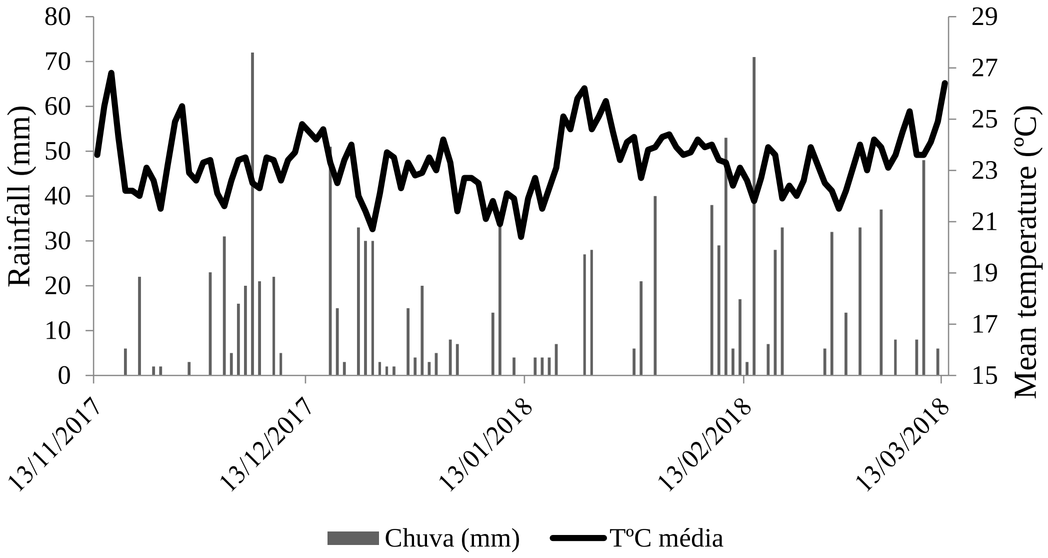
2. Material and Methods

The methodology adopted consisted of field experiment using quantitative methods (Pereira et al., 2008), in which the experimental data were collected and analyzed using statistical techniques

2.1. Conducting the experiment

The experiment was carried out in the experimental field of the Universidade Federal de Mato Grosso do Sul, Campus Chapadão do Sul (18°46'26"S, 52°37'28"W and an average altitude of 810m), municipality of Chapadão do Sul-MS, from November 2017 to February 2018. The climate of the region is humid tropical (Aw), characterized by dry winter and rainy summer, according to the Köppen classification. Figure 1 shows the climatic conditions during the experimental period with average rainfall and temperature over the experiment. Through the Figure, it can be seen that the prevailing climatic conditions were adequate for the crop development.

Figure 1. Climatic conditions during the experimental period.



Source: Developed by the authors based on data from Inmet (2018).

Three months before sowing, the soil base saturation of the experimental area was increased to 60% via liming. For the experiment installation, the soil was conventionally prepared by plowing, followed by two harrowing (clod-crusher and leveler). The rows were opened and fertilized using a John Deere®5 rows seeder, at a spacing of 0.45m between rows. The base fertilization consisted of 300kg ha^{-1} of the formulated 04-14-08. Seeds were manually sown, distributing 15 seeds per meter.

The experiment consisted of an augmented blocks design ($Y_{ij} = \mu + \tau_i + B_j + \varepsilon_{ij}$), using 196 lines and 10 controls, with five replications for each control. Table 1 shows the identification of the cultivars and their respective holding companies.

Table 1. Description of the cultivars used as control.

Cultivar	Owner	Cultivar	Owner
M 7211	Monsoy	1168	TMG
M 7908	Monsoy	123	TMG
M 9144	Monsoy	7262	TMG
NS 5959 IPRO	Nidera	UFVS Citrino	UFV
ST 815	Bayer	UFVS Turquesa	UFV

Source: Developed by the authors.

The experimental unit consisted of a 3m row for each line. Weeds, pests, and diseases control were carried out according to technical recommendations for the crop.

The following traits were evaluated: plant height (PH), number of days to flowering (NDF), and grain yield. NDF corresponded to the number of days between germination and maturation in more than 50% of plants in the plot. PH was evaluated by randomly selecting 15 plants in each experimental unit. Grain yield (GY, kg ha^{-1}) was estimated after harvesting each plot and correcting moisture to 13%.

2.2 Statistical analyses

Initially, data were subject to analysis of variance according to the statistical model $Y_{ij} = \mu + B_j + T_i + \varepsilon_{ij}$, in which: Y_{ij} is the value of the trait for the i-th treatment in the j-th block; μ is the overall mean; B_j is the effect of the j-th block; T_i is the effect of the i-th treatment, which can be decomposed into t_i: effect of the i-th control and P_i: effect of the i-th F_2 population; ε_{ij} is the random error.

The estimated genetic and environmental parameters were:

- Genotypic variance: $\hat{\sigma}_g^2 = \frac{QM_{treat} - QM_{res}}{r}$, where r refers to the number of blocks; QM_{treat} is the mean square of treatments; QM_{res} is the mean square of residue;

- Environmental variance: $\hat{\sigma}_e^2 = \frac{QM_{res}}{r}$;

- Phenotypic variance: $\hat{\sigma}_f^2 = \hat{\sigma}_g^2 + \hat{\sigma}_e^2$;

- Heritability: $h_g^2 = \frac{\sigma_g^2}{\sigma_g^2+\sigma_e^2}$;

- Coefficient of genotypic variation: $\mathrm{CV}_g(\%) = \left(\sqrt{\frac{\hat{\sigma}_g^2}{\mu}}\right) \times 100$, where μ is the overall mean;

- Coefficient of experimental variation: $\mathrm{CV}(\%) = \left(\sqrt{\frac{\hat{\sigma}_e^2}{\mu}}\right) \times 100$;

- b quotient: $b = \frac{\mathrm{CV}_g(\%)}{\mathrm{CV}\ \ (\%)}$.

The gain with direct selection (GS) on each trait was obtained by the expression: $GS = DS\frac{\hat{Cov}(X,Y)}{\sigma_{fx}^2}$, in which: DS: selection differential; Côv (X,Y): genetic covariance estimator between the individuals tested and the individuals from the improved population; σ_{fx}^2 : estimator of the phenotypic variance between the tested units.

Afterward, the Mulamba and Mock index (1978) was applied for simultaneous selection of traits, expressed by: $I = p_1r_1+p_2r_2+... + p_nr_n$, in which p_j is the economic weight assigned by the user to the j-th trait, where I is the index value for a given line; rj is the rank of this line in relation to the j-th trait; n is the number of traits considered in the index; p is the economic weights for each trait. For the establishment of these indices, two scenarios were considered: i) the use of the coefficient of genotypic variation of each trait, and ii) arbitrary weights, whose values were 1, 10, and 20 for the traits plant height, number of days to flowering, and grain yield, respectively.

All analyses were carried out in the Genes software (Cruz, 2013) and followed the procedures recommended by Cruz et al. (2012).

3. Results and Discussion

3.1. Genetic variability

The analysis of variance, according to the model of augmented blocks, is shown in Table 2.

Table 2. Summary of the analysis of variance for plant height (PH), number of days to flowering (NDF), and grain yield (GY) evaluated in 206 soybean genotypes grown in the Cerrado biome.

Source of variation	Degrees of freedom	Mean Square		
		PH	NDF	GY
Block	4	775.24	408.22	1188011.68
Treatment (Adjusted)	205	26.12*	50.51*	809686.76*
Residue	36	2.86	11.95	89806.94

*: significant at the 5% of probability by the F test. Source: Elaborated by the authors.

The F test indicated the significance of the treatments (genotypes) for the traits plant height (PH), number of days to flowering (NDF), and grain yield (GY). These results evidence the genetic variability in the population evaluated. Bárbaro et al. (2007), by evaluating five F_5 populations of soybean in the region of Jaboticabal, found significant differences for the same traits evaluated in this study.

The genetic and environmental parameters for the traits evaluated are shown in Table 3. The mean plant height and grain yield of the lines were higher than those of the controls. Conversely, the number of days to flowering was higher for the lines. Since the control genotypes were cultivars used in the market, results indicate the need for selecting the best lines of the evaluated population to meet the objective of soybean producers (early-cycle cultivars with high grain yield).

The overall coefficient of experimental variation of controls and lines was lower than 11% for all traits (Table 3). These results reveal good experimental precision according to Pimentel-Gomes et al. (2009). The magnitude observed for these parameters was similar to that observed by Costa et al. (2004), Farias Neto and Vello (2001), and Azevedo Filho (1998).

Table 3. Overall mean and mean of the controls and lines; overall coefficient of variation and coefficient of variation of controls and genotypes; estimates of phenotypic, genotypic, and environmental variances; heritability; coefficient of genotypic variation (CVg); and CVg/CV for (PH), number of days to flowering (NDF), and grain yield (GY) evaluated in 206 soybean genotypes grown in the Cerrado biome.

Parameter	PH	NDF	GY
Overall mean	46.09	49.39	2738.80
Mean – controls	45.32	47.04	2843.71
Mean – lines	46.28	49.99	2712.04
Overall CV (%)	3.67	7.00	10.94
Control CV (%)	3.74	7.35	10.54
Genotypes CV (%)	3.66	6.91	11.05
Phenotypic Variance	35.94	43.02	624211.39
Genotypic Variance	33.07	31.07	604404.45
Environmental Variance	2.87	11.95	89806.94
Heritability (%)	92.01	72.23	87.06
Genotypic CV (%)	12.42	11.15	28.66
Ratio CVg/CV	3.39	1.61	2.59

Source: Elaborated by the authors.

The phenotypic variance was close to the genotypic variance (Table 3) for plant height and grain yield, showing that the phenotype expressed is defined by the genotype. Therefore, the environmental variance showed low value for these traits but not for the trait flowering, which had a greater magnitude.

The environment (temperature, rainy days, photoperiod, among others) influenced the number of days to flowering. Board & Hall (1986), and Silveira Neto et al. (2005) verified that the interaction between the high nocturnal temperature and the photoperiod in short days influences the number of days to flowering in soybean.

The heritability value obtained for the traits plant height and grain yield (92.01 and 87.06, respectively) is considered as high, according to the classification of Resende (2002), Costa et al. (2004), and Farias Neto & Vello (2001) reported similar results in F_4:$_3$ and F_5:$_3$ populations, respectively. Diers et al. (2018) evaluated 5600 inbred soybean lines and reported heritability values for plant height, cycle, and hundred-grain weight similar to those observed in the present study.

The CVg/CV ratio is an indicator of the genetic potential of the population to obtain gains in each trait, and values higher than 1.0 are desirable. Costa et al. (2004) reported similar results in 1200 soybean genotypes in an augmented blocks design.

3.2. Genetic gains with selection

Table 4 shows the genetic gains with direct selection on the traits evaluated. The direct selection of shorter lines negatively affects the other traits, increasing the number of days to flowering and decreasing grain yield, which is not desirable.

Table 4. Estimate of the original mean (Xo), mean of selected genotypes (Xs), heritability (h^2), and selection gain (GS) obtained with direct selection for plant height (PH), number of days to flowering (NDF), and grain yield (GY) and the consequences observed on the other traits evaluated in 206 soybean genotypes grown in the Cerrado biome.

Selection method	Variable	Xo	Xs	h^2 %	GS	GS %
Direct on PH	PH	46.25	36.78	92.01	-8.71	-18.84
	NDF	49.71	50.81	72.23	0.79	1.6
	GY	2718.66	2695.01	87.06	-20.59	-0.76
Direct on NDF	PH	46.25	48.71	92.01	2.26	4.88
	NDF	49.71	37.30	72.23	-8.96	-18.03
	GY	2718.66	2212.50	87.06	-440.68	-16.21
Direct on GY	PH	46.25	46.45	92.01	0.19	0.40
	NDF	49.71	53.63	72.23	2.83	5.69
	GY	2718.66	4180.77	87.06	1272.97	46.82

Source: Elaborated by the authors.

Hamawaki et al. (2010) reported differences in PH of a population of soybean genotypes composed of 19 lines for the traits NDF and Y. Similarly, direct selection for fewer days to flowering increases plant height and decreases grain yield. No significant increase in plant height was provided by the selection for higher grain yield. However, the number of days to flowering increased. The means of the genotypes selected according to each direct selection strategy are shown in Tables S1, S2, and S3. Thus, the main objectives reported in this study (decrease in the number of days to flowering and increase in the grain yield) cannot be achieved with direct selection on any trait. These results indicate the need for the use of selection indices to identify the most suitable genotypes that will generate gains in the desired direction in all the traits.

The Mulamba and Mock index was used under two scenarios (Table 5). The first considered the coefficient of genotypic variation of each trait as economic weights; the second, assigned arbitrary weights to each trait (1, 10, and 20 for traits plant height, number of days to flowering, and grain yield, respectively). The use of the index in the first scenario resulted in no gains in all desirable directions since the number of days to flowering increased. However, in the second scenario, the Mulamba and Mock index selected soybean genotypes that carry the main desirable traits (decrease in number of days to flowering and increase in grain yield). The means of the genotypes selected, based on these two scenarios, are shown in Tables S4 and S5.

Table 5. Estimate of the original mean (Xo), mean of selected genotypes (Xs), heritability (h^2), and selection gain (GS) obtained with the Mulamba and Mock index (1978), using the coefficient of genotypic variation (CV) of each trait as economic weights and arbitrary weights for plant height (PH), number of days to flowering (NDF), and grain yield (Y); and the results on the other traits evaluated in 206 soybean genotypes grown in the Cerrado biome.

Economic Weight	Variable	Xo	Xs	h^2 %	GS	GS %
Genotypic CV	PH	46.25	42.24	92.01	-3.69	-7.97
	NDF	49.71	50.46	72.23	0.54	1.09
	Y	2718.66	3795.01	87.06	937.11	34.47
Arbitrary Weight	PH	46.25	48.43	92.01	2.01	4.34
	NDF	49.71	46.65	72.23	-2.21	-4.44
	Y	2718.66	3755.42	87.06	902.64	33.2

Source: Elaborated by the authors.

Costa et al. (2004) compared different selection criteria to evaluate 1200 soybean genotypes and reported that the Mulamba and Mock index provided the highest gains, confirming the efficiency of this index. The same result was observed by Bárbaro et al. (2007) when evaluating the genetic gain of five soybean populations in the F_5 generation for eleven traits of agronomic interest. Some authors used the Mulamba and Mock index in horticultural crops and obtained satisfactory genetic gains (Vasconcelos et al., 2010; Neves et al., 2011).

Obtaining desirable gains for number of days to flowering and grain yield is difficult because these traits have a negative genetic correlation. Hamawaki et al. (2010) evaluated 19 lines and found a negative correlation between these traits, as in the present study. Nogueira et al. (2012) evaluated the correlation between agronomic traits and reported that the phenotypic and genotypic correlation between these two variables is negative.

Therefore, the results obtained here are promising for soybean improvement, as they reveal the possibility of success in identifying genotypes that simultaneously combine earliness and high yield by using Mulamba and Mock index. Additionally, these genotypes can be used as genitors in crossbreeding blocks to obtain yielding and early genotypes, which are desirable characteristics for the Cerrado soybean improvers and farmers

4. Final Considerations

Direct selection does not generate genetic gains in the population regarding the decrease in number of days to flowering and increase in grain yield.

The Mulamba and Mock index associated with the use of the coefficient of genotypic variation for each trait as economic weight is not efficient in providing gains in the desired directions.

The use of arbitrary weights for the Mulamba and Mock index is effective for selecting early and yielding soybean genotypes for the Cerrado biome.

Future works evaluating other cultivars and in different sites of Brazil should be carried out, in order to contribute with more information about gains with selection in soybean crop.

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